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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/988,899A

DATE: 05/06/2003

TIME: 11:49:22

Input Set : A:\Dx003con.app

Output Set: N:\CRF4\05062003\I988899A.raw

3 <110> APPLICANT: HOOGENBOOM, HENDRICUS R.J.M.
 5 <120> TITLE OF INVENTION: NOVEL FAB FRAGMENT LIBRARIES AND METHOD FOR THEIR USE
 7 <130> FILE REFERENCE: DX/003 CON
 9 <140> CURRENT APPLICATION NUMBER: 09/988,899A
 10 <141> CURRENT FILING DATE: 2001-11-19
 12 <150> PRIOR APPLICATION NUMBER: PCT/US00/13682
 13 <151> PRIOR FILING DATE: 2000-05-18
 15 <150> PRIOR APPLICATION NUMBER: 99201558.6
 16 <151> PRIOR FILING DATE: 1999-05-18
 18 <160> NUMBER OF SEQ ID NOS: 71
 20 <170> SOFTWARE: PatentIn Ver. 2.1
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 23 <211> LENGTH: 11
 24 <212> TYPE: PRT
 25 <213> ORGANISM: Artificial Sequence
 27 <220> FEATURE:
 28 <223> OTHER INFORMATION: Description of Artificial Sequence: Illustrative
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 33 1 5 10
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 42 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
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 53 <220> FEATURE:
 54 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
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 60 <210> SEQ ID NO: 4
 61 <211> LENGTH: 17
 62 <212> TYPE: DNA
 63 <213> ORGANISM: Artificial Sequence
 65 <220> FEATURE:
 66 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer

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69 caggaaacag ctatgac
72 <210> SEQ ID NO: 5
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81 His His His His His His
82 1 5
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86 <211> LENGTH: 349
87 <212> TYPE: DNA
88 <213> ORGANISM: Artificial Sequence
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91 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
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94 <220> FEATURE:
95 <221> NAME/KEY: CDS
96 <222> LOCATION: (1)..(99)
98 <220> FEATURE:
99 <221> NAME/KEY: CDS
100 <222> LOCATION: (140)..(340)
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104 <222> LOCATION: (344)..(349)
106 <400> SEQUENCE: 6
107 tta ttc gca att cct tta gtt gtt cct ttc tat tct cac agt gca cag 48
108 Leu Phe Ala Ile Pro Leu Val Val Pro Phe Tyr Ser His Ser Ala Gln
109 1 5 10 15
111 gtc caa ctg cag gtc gac ctc gag atc aaa cgt gga act gtg gga gag 96
112 Val Gln Leu Gln Val Asp Leu Glu Ile Lys Arg Gly Thr Val Gly Glu
113 20 25 30
115 tgt taataaggcg cgccaattct atttcaagga gacagtcata atg aaa tac cta 151
116 Cys Met Lys Tyr Leu
117 35
119 ttg cct acg gca gcc gct gga ttg tta tta ctc gcg gcc cag ccg gcc 199
120 Leu Pro Thr Ala Ala Ala Gly Leu Leu Leu Ala Ala Gln Pro Ala
121 40 45 50
123 atg gcc cag gtg cag ctg cag gag agc ggg gtc acc gtc tca agc gcc 247
124 Met Ala Gln Val Gln Leu Gln Glu Ser Gly Val Thr Val Ser Ser Ala
125 55 60 65
127 tcc acc aaa tct tgt gcg gcc gca cat cat cat cat cac ggg gcc 295
128 Ser Thr Lys Ser Cys Ala Ala His His His His His His Gly Ala
129 70 75 80 85
131 gca gaa caa aaa ctc atc tca gaa gag gat ctg aat ggg gcc gca tag 343
132 Ala Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn Gly Ala Ala
133 90 95 100

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136 Thr Val
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150 1 5 10 15
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153 20 25 30
155 Cys
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169 1 5 10 15
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172 20 25 30
174 Val Ser Ser Ala Ser Thr Lys Ser Cys Ala Ala Ala His His His His
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177 His His Gly Ala Ala Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn
178 50 55 60
180 Gly Ala Ala
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281 <211> LENGTH: 23
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283 <213> ORGANISM: Artificial Sequence
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305 <211> LENGTH: 23
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307 <213> ORGANISM: Artificial Sequence
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310 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
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317 <211> LENGTH: 23
318 <212> TYPE: DNA
319 <213> ORGANISM: Artificial Sequence
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VERIFICATION SUMMARY

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